



LLCS/adm

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Dear Gene,

I am enclosing, on Joshua's request, a copy of the first issue of the newsletter "Taxometrics", giving available computer programmes for analysis of clusters in taxonomy. You can get a copy of future letters by writing to Mr. Hill.

I may add that S is a measure of similarity between two strains (or species) and is usually the % of characters that two strains have in common. In the case of our matrix, citations x cited, journals are roughly the equivalent of strains (species), and similarity may be taken as the % of cross citations. However, we have to resolve the asymmetrical matrix citing journal x cited journal into a symmetrical one as the matrix of S values is. Perhaps a first trial might be made by taking as S value, say between JAMA and AJHG the average between the % of citations found in JAMA which refer to AJHG papers, and the % of citations in AJHG which refer to JAMA papers. This is not ideal but at the moment I cannot imagine a better method. An analysis of the actual data would certainly be useful in this respect. The computer programme will then show which clusters can be formed out of journals. But I am afraid that none of the available programmes can handle a thousand journals.

I am therefore a little doubtful, from a superficial look at the programmes, that any of them will be useful as such. We are likely to develop new

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methods here, but it is hard to say how long it will take; probably longer than desirable from your point of view.

In the second half of September I will be able to contact my colleagues of the Computing Center here, who might be the best people to get in touch with for seeing what prospects there are of establishing a keypunching center here, and I will let you know something final about it.

All the best,

L.L. Cavalli-Sforza

C/to Prof. Lederberg